

ABSTRACT OF THE DISCLOSURE

Methods for identifying and controlling the genetic and metabolic pathways underlying complex phenotypes are provided. Conjoint polynucleotide segments that contribute to or disrupt elements of a multigenic phenotype are produced and expressed in cells of interest. Conjoint polynucleotide segments are recombined and/or mutated to give rise to libraries of recombinant concatamers which are expressed in cells of interest. Libraries of conjoint polynucleotide segments and recombinant concatamers are expressed episomally or integrated into the DNA of organelles or chromosomes. Cells are screened or selected to identify members of the population of cells exhibiting a desired phenotype. Libraries and vectors comprising conjoint polynucleotide segments and recombinant concatamers, as well as cells expressing such libraries and vectors or their components are provided. Kits containing conjoint polynucleotide segments, recombinant concatamers, vectors including such polynucleotides, and cells including such polynucleotides and vectors are provided.